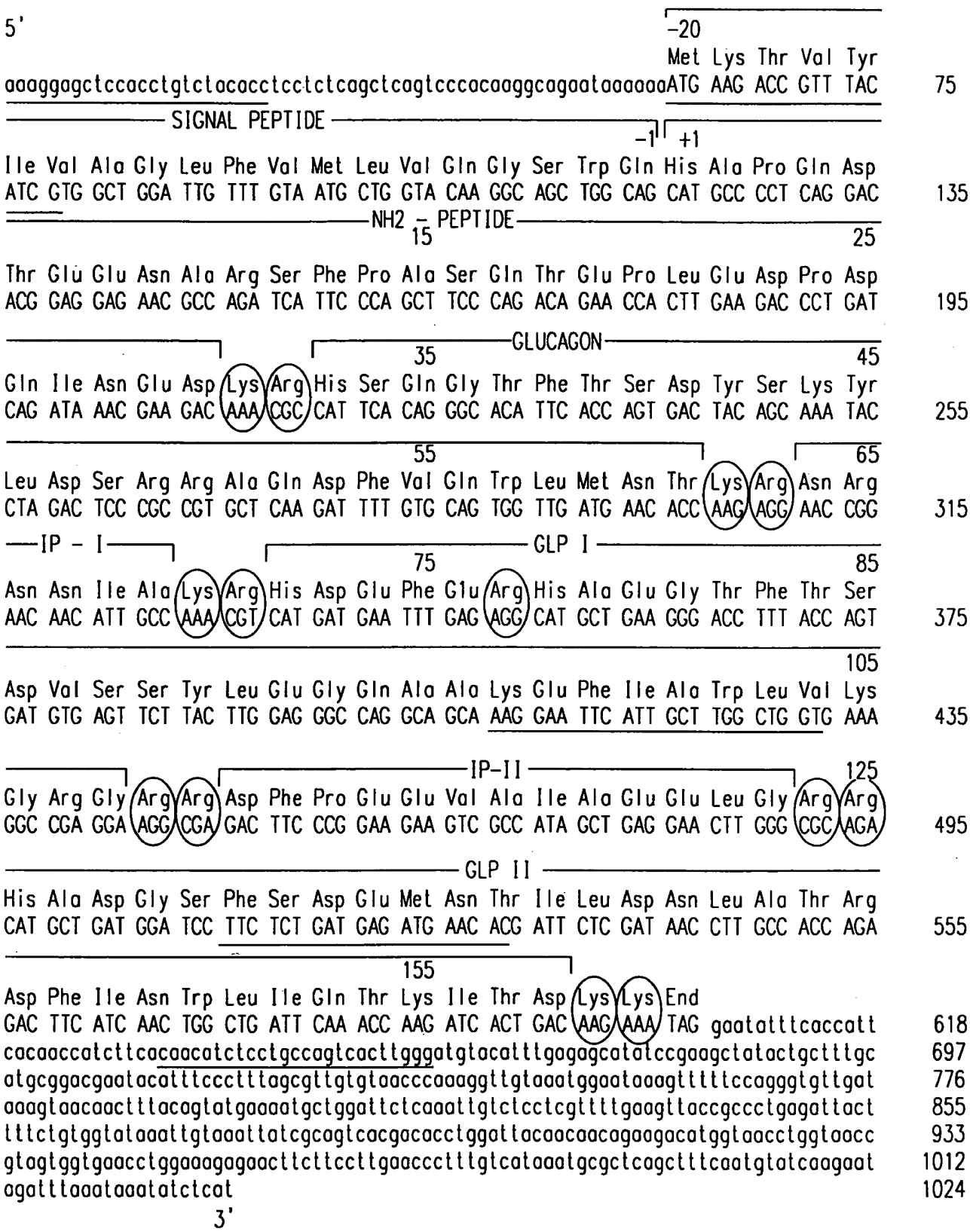
5'
-20
Met Lys Thr Val Tyr
aaaggagctccacctgtctacacctcctctcagctcagtcccacaaggcagaataaaaaaATG AAG ACC GTT TAC 75
SIGNAL PEPTIDE
-1 +1
Ile Val Ala Gly Leu Phe Val Met Leu Val Gln Gly Ser Trp Gln His Ala Pro Gln Asp
ATC GTG GCT GGA TTG TTT GTA ATG CTG GTA CAA GGC AGC TGG CAG CAT GCC CCT CAG GAC 135
NH2 - PEPTIDE
15 25
Thr Glu Glu Asn Ala Arg Ser Phe Pro Ala Ser Gln Thr Glu Pro Leu Glu Asp Pro Asp
ACG GAG GAG AAC GCC AGA TCA TTC CCA GCT TCC CAG ACA GAA CCA CTT GAA GAC CCT GAT 195
GLUCAGON
35 45
Gln Ile Asn Glu Asp Lys Arg His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr
CAG ATA AAC GAA GAC AAA CGC CAT TCA CAG GGC ACA TTC ACC AGT GAC TAC AGC AAA TAC 255
55 65
Leu Asp Ser Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr Lys Arg Asn Arg
CTA GAC TCC CGC CGT GCT CAA GAT TTT GTG CAG TGG TTG ATG AAC ACC AAG AGG AAC CGG 315
IP - I
GLP I
75 85
Asn Asn Ile Ala Lys Arg His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe Thr Ser
AAC AAC ATT GCC AAA CGT CAT GAT GAA TTT GAG AGG CAT GCT GAA GGG ACC TTT ACC AGT 375
105
Asp Val Ser Ser Tyr Leu Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys
GAT GTG AGT TCT TAC TTG GAG GGC CAG GCA GCA AAG GAA TTC ATT GCT TGG CTG GTG AAA 435
IP-II
125
Gly Arg Gly Arg Arg Asp Phe Pro Glu Glu Val Ala Ile Ala Glu Glu Leu Gly Arg Arg
GGC CGA GGA AGG CGA GAC TTC CCG GAA GAA GTC GCC ATA GCT GAG GAA CTT GGG CGC AGA 495
GLP II
His Ala Asp Gly Ser Phe Ser Asp Glu Met Asn Thr Ile Leu Asp Asn Leu Ala Thr Arg
CAT GCT GAT GGA TCC TTC TCT GAT GAG ATG AAC ACG ATT CTC GAT AAC CTT GCC ACC AGA 555
155
Asp Phe Ile Asn Trp Leu Ile Gln Thr Lys Ile Thr Asp Lys Lys End
GAC TTC ATC AAC TGG CTG ATT CAA ACC AAG ATC ACT GAC AAG AAA TAG gaatatttcaccatt 618
cacaaccatcttcacaacatctcctgccagtcacttgggatgtacatttgagagcatatccgaagctatactgctttgc 697
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gtagtggtgaacctggaaagagaacttcttccttgaacccttttgtcataaatgcgctcagctttcaatgtatcaagaat 1012
agatttaaataaatatctcat 1024
3'

FIG. 1